STM JOURNALS

International Journal of
Molecular Biotechnological Research

ISSN: 3107-3565
Volume 3, Issue 2, 2025
July–December
DOI (Journal): 10.37591/IJMBR

https://journals.stmjournals.com/ijmbr/

Research IJMBR

Exploring *Abies grandis* Phytocompounds' Potential by *In Silico* Analysis Targeting the 5P9J Protein

Vyomal Chaudhari[1,*], Jeni R. Patel[2]

Abstract

Blood Cancer, also popular with name "Hematologic cancer" have variety of types: Leukemia, Lymphoma, Myeloma, uncontrolled multiplication of blood cells mainly affecting to bone marrow and blood cells (White Blood Cells). Lymphoma, originating from lymphatic system resulted in uncontrolled growth and instead of normal apoptosis development of tumor. Myeloma, uncontrolled formation of malignant plasma cells leads to disrupting production of healthy blood cells. This situation creates variety of diseases like anemia, thrombocytopenia, and leukopenia. Leukemia and lymphomas involved abnormal growth and survival of cancerous blood cells resulted due to mutation in RAS signaling. 5p9j protein (RAS protein, a small GTPase molecule) is responsible for this mutation in signaling pathway. To cure these types of diseases, In Silico analysis using multi-target molecular docking method was used. In present study, total 13 bioactive compounds of source medicinal plant named Abies grandis were used to explore top three phytocompounds and their anticancer potential against malignant activity of 5p9j protein.

Keywords: Molecular docking, RAS signaling, *Abies grandis*, Lymphoma, Myeloma, SwissADME analysis, Biovia Discovery studio visualization

INTRODUCTION

Blood Cancer is worldwide issue related to human health. Blood Cancer resulted from the mutation of RAS signaling includes various types like Leukemia and Lymphoma [1]. Generally, protein is known as Human Mutant RAS Complex and on PDB database protein complex is represented as 5P9J (PDB ID) [2]. Protein is responsible for uncontrolled cell proliferation, programmed cell death and tumor formation and other problems of blood cells due to mutation in RAS signaling [3–5]. RAS complex plays important role in two major MAPK/ERK pathways (responsible for cell growth promotion, proliferation and survival) and PI3K/AKT pathway (responsible for cell survival and apoptosis resistance) [6, 7]. Due to mutation in RAS complex [8], it causes tumorgenesis, chemo-resistance and metastasis. So, targeting RAS signaling becomes an important topic to investigate solutions for curing the above mentioned cancer types. Here, like other many conifers, *Abies grandis* has a variety of bioactive compounds holding potential for modulating cancer related pathways, mainly those influenced by mutant RAS signaling [5]. Each of the compounds have their own biological activities that may be effective against malignant cell growth, survival and metastasis. RAS inhibition therapy, MEK inhibition therapy and PI3K/AKT inhibition therapy are the trending treatments for RAS driven cancers [9]. But there are some limitations or less chances to be effective due to mutation specificity, Resistance against targeted therapies, toxicity and RAS driven cancers exhibit immune resistance [10]. In present, bioactive compounds retrieved from online databases (from IMPPAT, PubChem database and PDB). Total 13 compounds were used for the molecular docking study against targeted

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Received Date: May 21, 2025
Accepted Date: July 06, 2025
Published Date: September 15, 2025

Citation: Vyomal Chaudhari, Jeni R. Patel. Exploring *Abies grandis* Phytocompounds' Potential by *In Silico* Analysis Targeting the 5P9J Protein. International Journal of Molecular Biotechnological Research. 2025; 3(2): 1–12p.

5P9J protein [11, 12]. Followed by pharmacokinetic screening by using several parameters like Lipinski's rule of "0" violation, high gastro-intestinal absorption, high bioavailability [13]. Then after, target protein purification and molecular docking analysis and visualization were performed [14]. By using *Abies grandis* as a source plant, its phytocompounds were explored and *In Silico* analyzed their efficiency as a therapeutic agent for lymphatic and leukemic blood cancer [15–17].

METHODOLOGY

Retrieval of Ligands

The information of 13 bioactive compounds was retrieved from the online IMPPAT database (https://cb.imsc.res.in/imppat/). This database provides a massive collection of data related to phytochemicals, their bioactivity and toxicological properties. All types of data were collected from medicinal plants. So, this database is considered as primary source of bioactive compounds in present study. All 13 bioactive compounds' necessary information was downloaded with their canonical smiles, from PubChem CID (Table 1) and 3D structure in SDF format from the PubChem database (https://pubchem.ncbi.nlm.nih.gov/) from source plant "*Abies grandis*".

Retrieval of Protein

The target protein, known as RAS protein, was the major target for drug discovery in cancer therapy. To inhibit the mutant forms of RAS protein, target protein molecule "5P9J" was retrieved and downloaded as .pdb file from the Protein Data Bank (PDB) (https://www.rcsb.org/?ref=-nav_home) for further analysis. Retrieved target protein had structural components, like KRAS (Kirsten rat sarcoma viral oncogene homolog) having specific mutation at 12th position, where glycine is substituted with cysteine.

Protein Purification

The protein having three "A" chains, was retrieved from the PDB database (https://www.rcsb.org/) and was further purified by removing other molecules like heteroatom's, water molecules, and ligand groups. Then polar hydrogen's were added to correct protonation state, improved molecular interaction if polar residues forming H-bonds, ensuring charge distribution. Finally, purified protein molecules are ready for further docking analysis. This targeted protein requires purification process to remove unwanted components from the structure for further analysis. This structure will be used to predict interactions with selected different bioactive compounds in molecular docking analysis. The entire process was done using Biovia Discovery Studio 2024 software [18].

In Silico Pharmacokinetic Analysis and Screening of Ligands

For molecular docking, ligand molecules also required to interact with purified protein molecules to get information like their binding affinity and other predictions. Phytocompounds mentioned in Table 1 were analyzed by using SwissADME tool (http://www.swissadme.ch/) to evaluate or predict their pharmacokinetic properties and to support identifying drug likeliness.

Top 6 bioactive compounds were selected based on several parameters like Lipinski's rule of "0" violation, high gastro-intestinal absorption, high bioavailability for further analysis. Details are given in Table 2.

Molecular Docking of Protein and Ligands

Molecular docking analysis was performed by using target protein 5P9J and 6 screened ligand molecules having suitable parameters in PyRx tool [11]. Top 3 ligands having highest binding affinity were taken for further analysis. Those top 3 ligands named "Geranyl acetate", "alpha-TERPINEOL", and "Citronellyl acetate" were taken for further analysis.

Visualization of Docked Molecules

These top 3 molecules were visualized using Biovia Discovery Studio as docked molecules with target protein 5P9J. Two of them show excellent binding with target proteins binding sites given in results (Figures 1-3). 3D and 2D visualization carried out to predict the binding possibilities [14].

Visualization of Conserved Regions

Using Consurf online tool (https://consurf.tau.ac.il/), conserved residue analysis was done by Rate4sites Bayesian method. High resolution figure and per residue details were analyzed.

RESULTS

Retrieval of Protein and Purification

5P9J a Protein Data Bank entry (PDB ID) represents crystal structure of BTK complex (Bruton's Tyrosine Kinase) with "ibrutinib". Inhibitors are covalently bounded with BTK enzyme. Ribbon, like target protein 5P9J having 32.77 kDa molecular weight from human, was used to analyze anticancer potential of top 3 bioactive compound. X-ray diffraction method was used to determine molecules. The resolution of protein is 1.08 Å. Protein structure is a single polypeptide chain "A" comprises of 263 amino acids, corresponding to residues 382-659 of the full BTK protein. Purified form contains only "A" chain and polar groups having well distributed charge. 219 residues are present in "A, B, L" regions. 176 hetero groups were present in this structure (Figure 1). Here, according to Ramachandran plot analysis, a good quality model expected over 90% in the most favored regions [A, B, L]. Moreover, another expected Ramachandran plot statistics & plot given below:

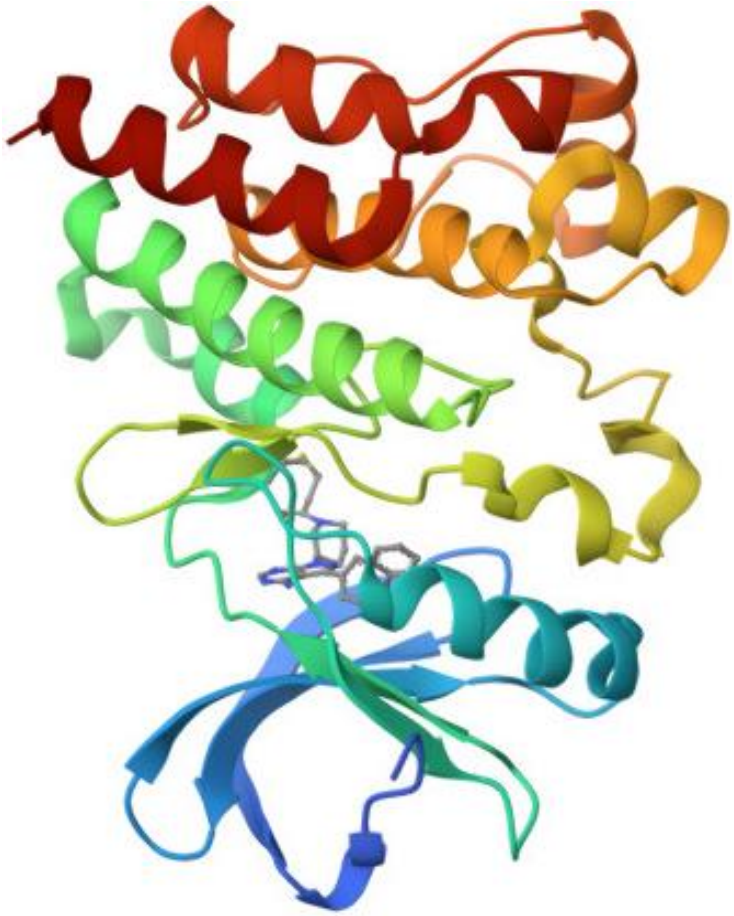

Figure 1. 3D Structure of 5P9J Protein with "ibrutinib" inhibitor.

Structural validation reports were distributed in two major representations: (a) Global Validation Metrics, and (b) Comparative table. R_{free} ranking shows models' good fit. Clash score is near 0, which shows minimal clashes and unfavorable regions. Ramachandran outliers 0% means all residues fall within allowed region. RSRZ outliers are low, which indicates good agreement between model and data. Among the other structure entries, 5P9J ranks best structure in terms of geometrical and refinement. These results for protein prove best suitability for the molecular docking analysis.

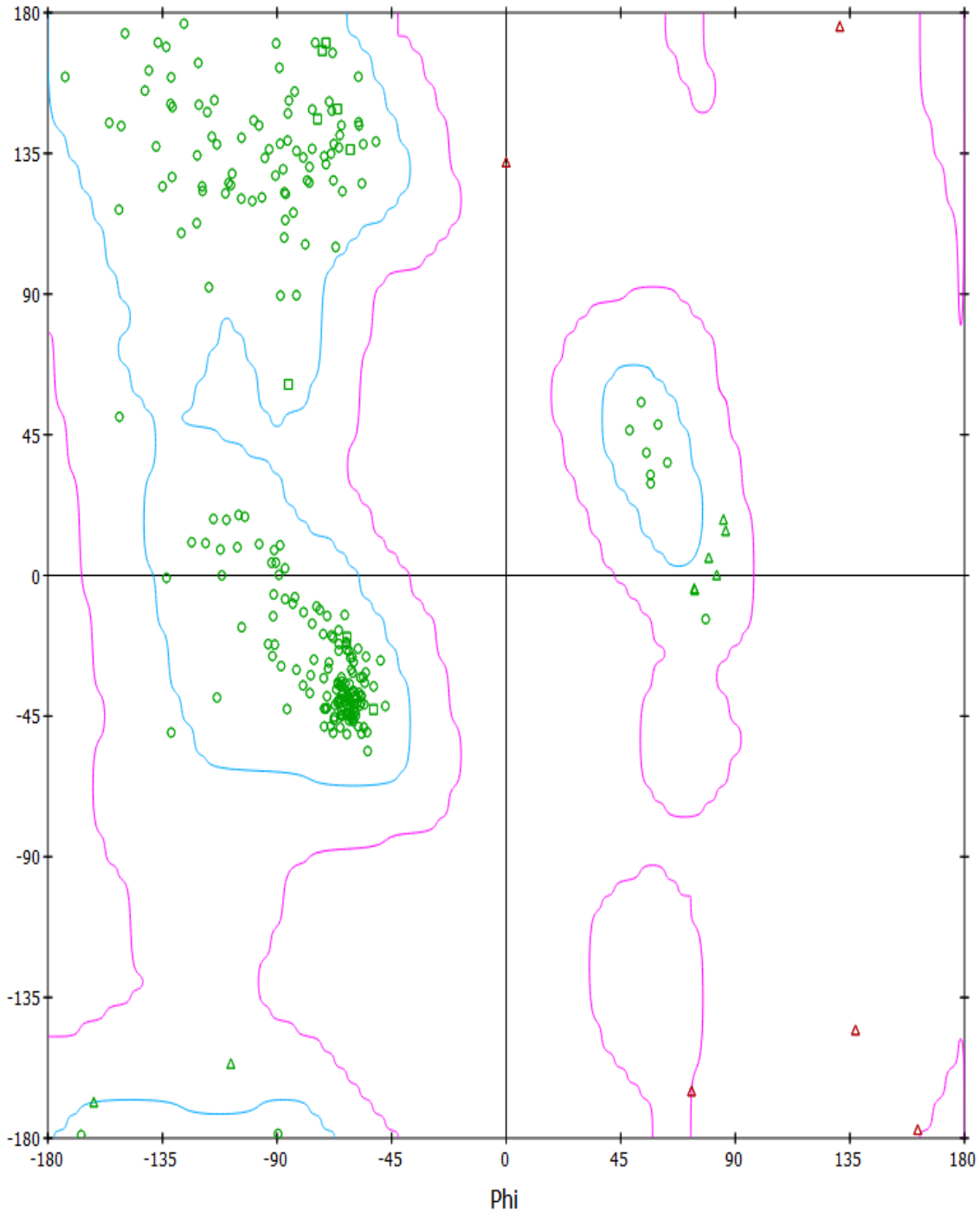

Figure 2a. Ramachandran plot of 5P9J protein showing the distribution of backbone dihedral angles (φ and ψ) for non-glycine, non-proline residues.

Ramachandran plot (Figure 2a) indicates that 92% of residues fall within the most favored regions coded as red, brown, and yellow.

In Ramachandran plot (Figure 2b), blue contour lines represent allowed or favored regions and pink contour lines represent additional allowed regions. Non-glycine and non-proline residues are represented as small green circles. Triangles are red in color represent structural issues in molecules. Green triangles indicate glycine residues. Plot indicates excellent stereochemistry of target molecules.

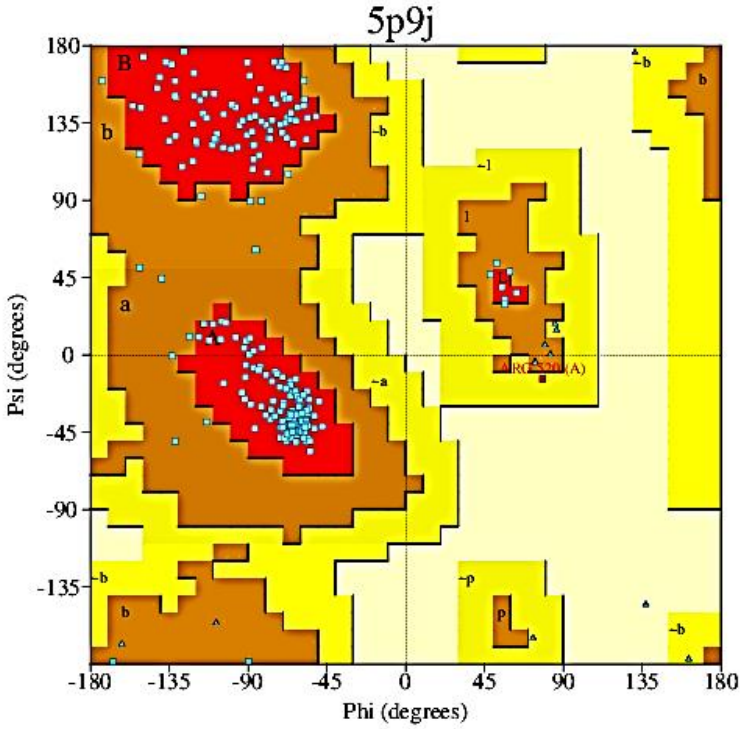

Figure 2b. Ramachandran plot showing stereochemistry of target molecule.

Table 1. Summarized validation provides details of 5p9j protein.

Category	Results	Observation
Basic information	Resolution (X-ray): 1.08 Å	Very high-quality resolution.
Overall score	Clash score:2 Ramachandran outliers: 0% Sidechain outliers: 0%	Excellent geometry.
R-factors	R-work:0.209 R-free: 0.224	Good, R-free within ~5% of R-work.
Completeness	82.3%	Slightly low, but acceptable.
Protein Chains	Chain A:263 residues, 2161 atoms	Well modelled.
Ramachandran plot	Favored: 98% Allowed: 2% Outliers: 0%	Excellent backbone conformation.
Sidechains	Outliers: 0% (all aromatic)	Very good.
Geometry Outliers	Bond length: 0.3% (6/2211) Bond angles: 0.4% (13/2986)	Mirror deviations.
Planarity / Chirality	Planarity outliers: 1 Chirality outliers: 0	Negligible.
Clashes	7 intra-unit clashes	Low clash score = Good.
B-factors (protein)	Average B: 19 $Å^2$	Low = stable model.
RSRZ outliers (fit to density)	10 residues (~3%) non symmetry related	Acceptable for high resolution.
Ligand–Ibrutinib analog	Atoms: 33 RSCC: 0.94 (Good fit) RSR: 0.07 (Excellent fit) B-factors: 12–23 $Å^2$ Bond length outliers: 4 Bond angle outliers 8 Torsion outliers: 4	Ligands fit well but have some geometry outliers.
Waters	175 water molecules included	Well defined.
Overall Assessment	High quality structure	Minor ligand geometry issues only. Therefore, reliable for docking/interaction analysis.

Table 2. Compounds name, PubChem CID and Canonical smiles of bioactive compounds from the source plant "*Abies grandis*".

Compound Name	PubChem CID	Canonical Smile
1. Myrcene	31253	CC(=CCCC(=C)C=C)C
2. Tricyclene	79035	CC1(C2CC3C1(C3C2)C)C
3. Citronellyl acetate	9017	CC(CCC=C(C)C)CCOC(=O)C
4. Borneol	6552009	C[C@@]12CC[C@@H](C1(C)C)C[C@@H]2O
5. Geranyl acetate	1549026	CC(=CCC/C(=C/COC(=O)C)/C)C
6. (+)–Beta–Phellandrene	442484	CC(C)[C@@H]1CCC(=C)C=C1
7. Camphor	2537	CC1(C2CCC1(C(=O)C2)C)C
8. Alpha–PINENEsx	6654	CC1=CCC2CC1C2(C)C
9. Beta–Pinene	14896	CC1(C2CCC(=C)C1C2)C
10. Alpha–Terpineol	17100	CC1=CCC(CC1)C(C)(C)O
11. Bornyl acetate	93009	CC(=O)O[C@@H]1C[C@@H]2CC[C@]1(C2(C)C)C
12. Camphene	6616	CC1(C2CCC(C2)C1=C)C
13. Limonene, (+/–)–	22311	CC1=CCC(CC1)C(=C)C

Retrieval and Pharmacological Studies of the Compounds

In SwissADME pharmacokinetic analysis of bioactive compounds, three major important parameters were used to screen out bioactive compound having drug likeliness. Lipinski's 0 violation rule, high GI absorption, high bioavailability, BBB permeant like parameters were used and by using these physicochemical parameters, total six bioactive compounds Citronellyl acetate, Borneo, Geranyl acetate, Camphor, alpha Terpineol, bornyl acetate were screened out of 13 Phytocompounds of *Abies grandis* (Table 3).

Table 3. SwissADME analysis by considering physicochemical parameters.

Molecule	PubChem CID	MW	Lipinski violations	GI absorption	Bioavailability score
Citronellyl acetate	9017	198.3	0	High	0.55
Borneol	6552009	154.25	0	High	0.55
Geranyl acetate	1549026	196.29	0	High	0.55
Camphor	2537	152.23	0	High	0.55
Alpha Terpineol	17100	154.25	0	High	0.55
Bornyl acetate	93009	196.29	0	High	0.55

Physicochemical properties, like molecular weight, H-Bond donors (HBD), H-Bond acceptors, TPSA (Topological Polar Surface Area), LogP (XLogP, etc.), and water solubility, were explored. Obtained results given in Tables 4 and 5.

Table 4. ADME & drug likeness profile.

S.N.	Parameter	Geranyl acetate	α-Terpineol	Citronellyl acetate
1	Molecular formula	$C_{12}H_{20}O_2$	$C_{10}H_{18}O$	$C_{12}H_{20}O_2$
2	Molecular weight (MW)	196.29 g/mol	154.25 g/mol	198.30 g/mol
3	Heavy atoms	14	11	14
4	Rotatable Bonds	6	1	7
5	H-Bond Donors (HBD)	0	1	0
6	H-Bond Acceptors (HBA)	2	1	2
7	TPSA ($Å^2$)	26.30	20.23	26.30
8	LogP (Consensus)	3.30	2.58	3.46
9	Water solubility (ESOL)	–3.21	–2.87	–3.43
10	GI absorption	High	High	High
11	BBB permeation	Yes	Yes	Yes
12	P-gp Substrate	No	No	No

13	CYP inhibitions	Not a strong inhibitor for CYP1A2, 2C9, 2C19, 2D6, 3A4	Not a strong inhibitor for CYP1A2, 2C9, 2C19, 2D6, 3A4	Not a strong inhibitor for CYP1A2, 2C9, 2C19, 2D6, 3A4
14	Skin permeability (Log *Kp*) cm/s	–4.63	–4.83	–4.33

Table 5. Drug likeness evaluation.

S.N.	Parameter	Geranyl acetate	α-Terpineol	Citronellyl acetate
1	Lipinski	Pass	Pass	Pass.
2	Ghose	Pass	1 violation: MW	Pass.
3	Veber	Pass	Pass	Pass.
4	Egan	Pass	Pass	Pass.
5	Muegge	1 violation	2 violations	1 violation.
6	PAINS Alert	0 alert	0 alert	0 alert.
7	Lead likeness	2 violations	1 violation	2 violations.
8	Bioavailability	0.55	0.55	0.55
9	Synthetic Accessibility	2.72	3.24	2.69

Boiled egg visualization (Figures 3 and 4) proves that all molecules fall within the yellow region (BBB-permeant) suggesting that they have high CNS permeability and may act on brain targets. All molecules in red indicate that they are not actively effluxed by P-glycoprotein and can passively be diffused.

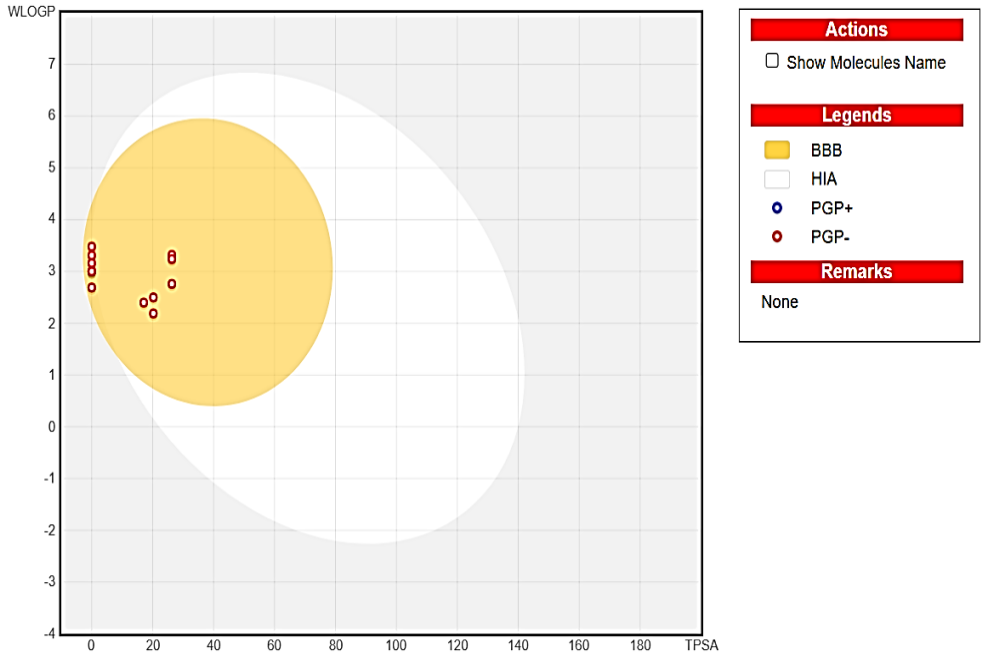

Figure 3. Boiled egg analysis of phytocompounds.

Molecular Docking Analysis and Visualization

Visualization of docked molecules 2D and 3D visualization was carried out. According to Figure 4, Geranyl acetate interacts with amino acid ASP426, amino acid TYR461, amino acid TYR476, creates H-bonds and other molecular interactions with target protein. Citronellyl acetate is showing interaction with GLU475, GLN459, TYR461 and ASP426. It shows little bit similarity to Geranyl acetate but binding affinity is possibly different. Alpha Terpineol shows Van der Val interactions only with target protein and weaker binding affinity (Table 6).

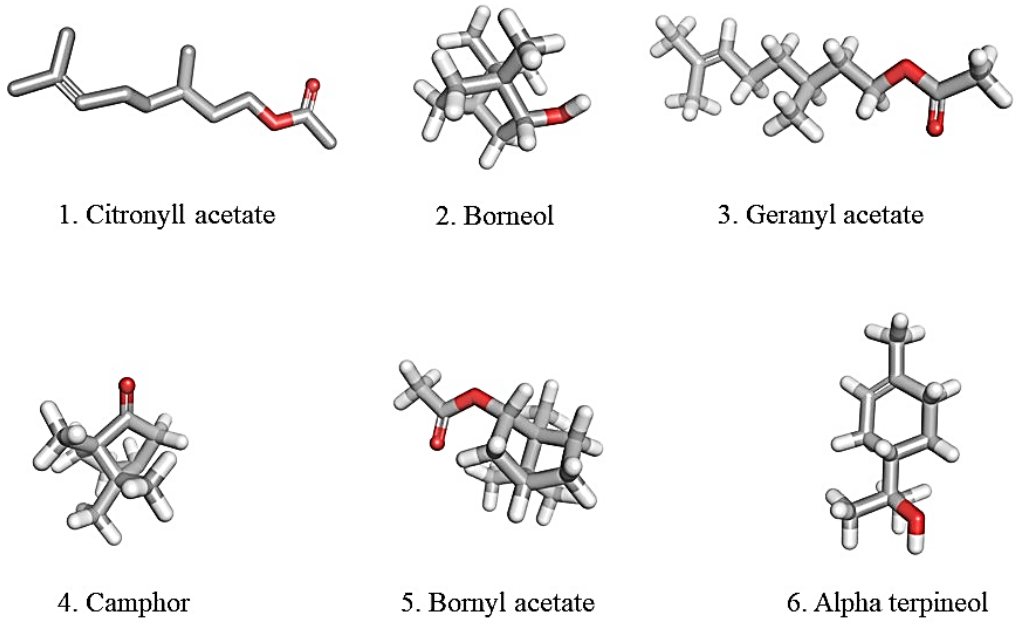

Figure 4. Structure of bioactive compounds retrieved and selected for molecular docking from medicinal plant "*Abies grandis*".

Table 6. Statistics of total residues and conserved residues.

Total number of residues	Number of conserved residues	Percentage of conserved residues
180	57	31.67 %

DISCUSSION

Here, 5P9J protein is popular target for mutation induced anticancer solutions in lymphoma and myeloma disease. It is co-crystallized structure of Bruton's Tyrosine Kinase and inhibitor ibrutinib. BTK plays important role in B-cell receptor signaling and development, functioning of B-cells. Mutations in BTK are associated with B-cell malignancies. Ibrutinib is a covalent inhibitor that binds irreversibly to BTK and blocks its activity. This inhibition disrupts downstream pathway of signaling and leads B-cell malignancies such as mantle cell lymphoma, chronic lymphocytic leukemia, and waldenstrom's macroglobulinemia [19, 20]. Present study reveals molecular interactions between protein 5P9J and three terpene derived compounds: Geranyl acetate, Citronellyl acetate, Alpha Terpineol (Table 7).

Ramachandran plot explains protein's stereochemistry is excellent due to almost majority of the residues are in favored and allowed region. Very few outliers indicated that protein structure is well defined. Figure 2 RSRZ outliers indicates minor deviations but in acceptable range. The data represents high quality crystallographic model and is highly reliable.

Geranyl acetate has potential anticancer activity, antioxidant activity, antimicrobial and anti-inflammatory activity. With Geranyl acetate, three amino acid residues Asp-426, Tyr-461, and Tyr-476 shows interaction. There was pi alkyl interaction between geranyl acetate and TYR A-461 so hydrophobic stabilization occurs. Potential steric hindrance was noticed due to unfavorable bumps. Potential hydrogen bonding between residue (Asp-426, Tyr-476) electrostatic interactions suggest stability enhancement (Figures 5-7).

Citronellyl acetate was involved in B-cell Malignancies. Citronellyl acetate shows bonding with Asp-426, Tyr-461, Tyr-476, Val-427 and Glu-475 by Van Der Val forces. Just same as Geranyl acetate but different orientation and strength. Very less interaction occurred by Van der Val bond with Gln-459,

proves lower binding affinity as compared with above two compounds. Because they exhibit great binding potential due to multiple binding of residue. Chemical modifications might improve their binding affinity for better therapeutic potential.

Table 7. Ligands and their stability potential.

Ligand	Key interacting residues	Binding efficiency	Binding energy (kcal/mol)	Stability potential
Geranyl Acetate	Asp-426, Tyr-461, Tyr-476	Moderate to strong	–6.3	Moderate.
Citronellyl Acetate	Asp-426, Tyr-461, Tyr-476, Val-427	Stronger	–5.9	Higher stability.
Alpha Terpineol	Gln-459	Weaker	–6.4	Lower stability.

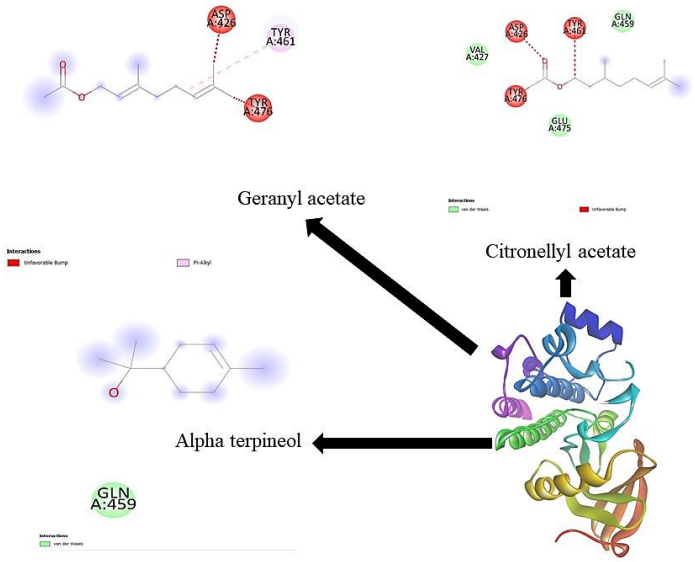

Figure 5. 2D Molecular docking results of 5P9J protein and three bioactive compounds, Geranyl acetate, Citronellyl acetate and Alpha Terpineol.

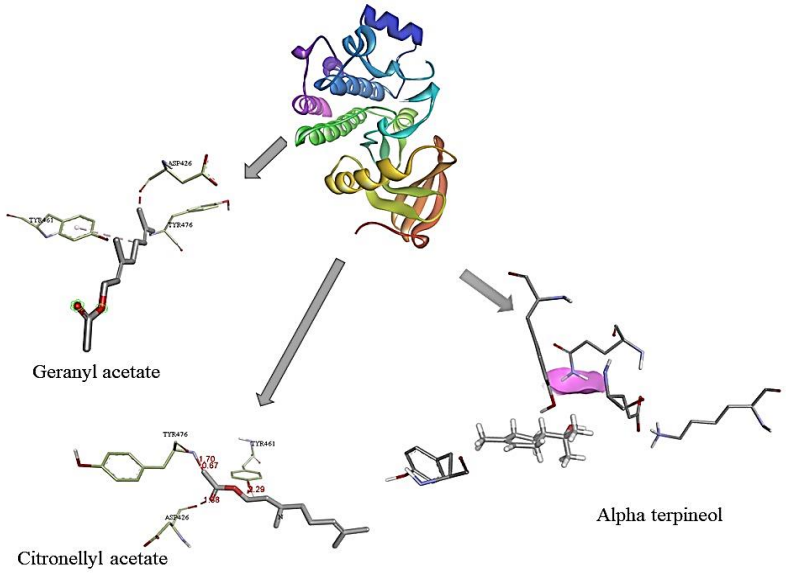

Figure 6. 3D Visualization of ligands and protein's reaction after molecular docking.

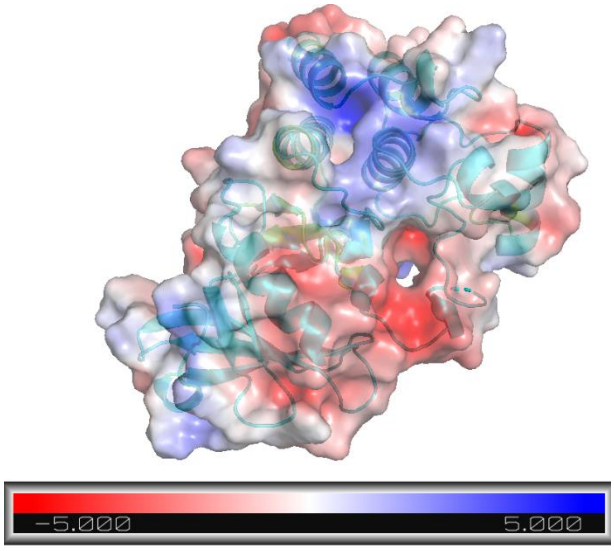

Figure 7. Electrostatic potential of 5P9J molecule.

CONCLUSIONS

Present analysis shows moderate interactions between target protein 5P9J and three terpene derived compounds: Geranyl acetate, Citronellyl acetate, Alpha Terpineol. Interactions were there with Geranyl acetate and Citronellyl acetate compounds but not sufficiently as required.

The molecular docking of Geranyl acetate, Citronellyl Acetate and Alpha Terpineol against the target protein highlights their potential binding efficiency and interaction mechanisms. Here, citronellyl demonstrated the strongest binding affinity due to multiple interactions with key residues, contributing to a more stable complex. The presence of hydrogen bonds and van der Waals forces indicates that Citronellyl Acetate may serve as a promising compound for further biological evaluation. Geranyl Acetate also exhibited moderate binding, interacting with Asp426, Tyr461 and Tyr476. Presence of steric clashes may reduce its overall stability. Structural modifications, like addition of polar functional groups, could enhance its binding potential. Alpha terpineol showed the weakest interactions with target protein forming only van der Waals interaction with Gln459 indicating a lower affinity to the protein.

Binding results indicate that Citronellyl Acetate may have possible better inhibitory potential against the target protein. It makes more suitable bioactive compound for drug development studies. In addition, more analysis is required, like binding free energy calculations, molecular dynamic simulations, and in vitro assays, to confirm their biological activity and therapeutic potential.

Abies grandis have mainly two effective compounds Citronellyl Acetate and Geranyl Acetate showed satisfactory results with target protein.

By exploring pharmacokinetic analysis and molecular docking analysis, Citronellyl Acetate is emerging as most promising ligand or bioactive compound from the source plant *Abies grandis*.

ABBREVIATIONS

GTPas	**Guanosine tri-phosphatase.**
RAS	Rat Sarcoma.
PDB	Protein Data Base.
MAPK	Mitogen Activated Protein Kinase.
ERK	Extracellular Signal Regulated Kinase.
PI3K	Phosphoinositide 3-kinase.

AKT	AK strain Transforming.
IMPPAT	Indian Medicinal Plants, Phytochemistry and Therapeutics.
CID	Compound Identifier.
SDF	Structure Data File.
RSRZ	Real Space R- Value Z-Score.
SwissADME	Swiss Absorption, Distribution, Metabolism, and Excretion.
BTK	Bruton's Tyrosine Kinase.
2D	Two Dimensional.
3D	Three Dimensional.
ASP	Aspartate.
TYR	Tyrosine.
GLU	Glutamate.
GLN	Glutamine.

REFERENCES

1. Vojtek AB, Der CJ. Increasing complexity of the Ras signaling pathway. J Biol Chem. 1998;273(32):19925–8.
2. Sussman JL, Lin D, Jiang J, Manning NO, Prilusky J, Ritter O, et al. Protein Data Bank (PDB): Database of three-dimensional structural information of biological macromolecules. Acta Crystallogr D Biol Crystallogr. 1998;54(6):1078–84.
3. Li S, Balmain A, Counter CM. A model for RAS mutation patterns in cancers: Finding the sweet spot. Nat Rev Cancer. 2018;18(12):767–77.
4. Rojas JM, Santos E. Ras genes and human cancer: Different implications and different roles. Cancer Gene Ther. 2002;3(4):295–311.
5. Wittinghofer A, Waldmann H. Ras—A molecular switch involved in tumor formation. Angew Chem Int Ed Engl. 2000;39(23):4192–214.
6. Sun Y, Liu WZ, Liu T, Feng X, Yang N, Zhou HF. Signaling pathway of MAPK/ERK in cell proliferation, differentiation, migration, senescence and apoptosis. J Recept Signal Transduct Res. 2015;35(6):600–4.
7. Burotto M, Chiou VL, Lee JM, Kohn EC. The MAPK pathway across different malignancies: A new perspective. Cancer. 2014;120(22):3446–56.
8. Prior IA, Lewis PD, Mattos C. A comprehensive survey of Ras mutations in cancer. Cancer Res. 2012;72(10):2457–67.
9. Ryan MB, Corcoran RB. Therapeutic strategies to target RAS-mutant cancers. Nat Rev Clin Oncol. 2018;15(11):709–20.
10. Yang H, Liang SQ, Xu D, Li X, Li M, Song X, et al. Targeting RAS mutants in malignancies: Successes, failures, and reasons for hope. Signal Transduct Target Ther. 2023;43(1):42–74.
11. Dallakyan S, Olson AJ. Small-molecule library screening by docking with PyRx. Methods Mol Biol. 2015;243–50.
12. Pawar RP, Rohane SH. Role of AutoDock Vina in PyRx molecular docking. J Drug Deliv Ther. 2021;11(4):1–5.
13. Daina A, Michielin O, Zoete V. SwissADME: A free web tool to evaluate pharmacokinetics, drug-likeness and medicinal chemistry friendliness of small molecules. Sci Rep. 2017;7(1):42717.
14. Baroroh U, Fadhilah R, Anggraini F, Alimi R, Fadly D. Molecular interaction analysis and visualization of protein–ligand docking using Biovia Discovery Studio Visualizer. Indones J Pharm Sci Technol. 2023;2(1):22–30.
15. Bhardwaj K, Saini S, Choudhary N, Singh R, Singh J. Conifers phytochemicals: A valuable forest with therapeutic potential. Pharmacogn Rev. 2021;26(10):3005–12.
16. Rho HS, Jeong HG, Kim DH, Chang MS, Chung JH. Mechanism of NF-κB activation induced by γ-irradiation in B lymphoma cells: Role of Ras. Int J Radiat Biol. 2005;81(23-24):2019–31.
17. Seibold M, Schnizler K, Schoenherr C, Schneider B, Lutz C, Wrobel G, et al. RAL GTPases mediate multiple myeloma cell survival and are activated independently of oncogenic RAS. Haematologica. 2019;105(9):2316–24.

18. Pawar SS, Rohane SH. Review on Discovery Studio: An important tool for molecular docking. J Drug Deliv Ther. 2021;11(3):48–54.
19. Buggy JJ, Elias L. Bruton tyrosine kinase (BTK) and its role in B-cell malignancy. Immunol Rev. 2012;246(2):119–32.
20. Satterthwaite AB, Li Z, Witte ON. Btk function in B cell development and response. Semin Immunol. 1998;10(4):309–16.

